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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:02 ; Search time 46.589 Seconds
(without alignments)
420.957 Million cell updates/sec

Title: US-08-325-278B-1_COPY_5_80
Perfect score: 389
Sequence: 1 KEETPTPTDSEEVITIKAFANGSTOTAFKGTFEKATSEAYADTLKKNGET 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Maximum DB seq length: 0
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:

- 1: sp_archaea:
- 2: sp_bacteria:
- 3: sp_fungi:
- 4: sp_human:
- 5: sp_invertebrate:
- 6: sp_mammal:
- 7: sp_mhc:
- 8: sp_organellae:
- 9: sp_phage:
- 10: sp_plant:
- 11: sp_rodent:
- 12: sp_virus:
- 13: sp_vertebrate:
- 14: sp_unclassified:
- 15: sp_rvirus:
- 16: sp_bacteriaph:
- 17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	389	100.0	455	2 Q53291	Q53291 streptococ
2	389	100.0	719	2 Q51912	Q51912 peptostrept
3	298.5	76.7	992	2 Q51918	Q51918 peptostrept
4	85	21.9	1576	16 Q825V8	Q825V8 yersinia pe
5	74	19.0	529	1 Q48937	Q48937 methanosarc
6	73.5	18.9	451	2 Q924J9	Q924J9 lactobacill
7	72	18.5	477	10 Q932G9	Q932G9 arabisdopsis
8	72	18.5	487	10 Q9STK2	Q9STK2 arabisdopsis
9	71.5	18.4	947	2 Q86487	Q86487 staphylococ
10	71	18.3	528	16 Q9KX8	Q9KX8 bacillus ha
11	71	18.3	929	3 P78718	P78718 nectria hae
12	70.5	18.1	955	16 Q8NXX7	Q8NXX7 staphylococ
13	70	18.0	645	5 Q33862	Q33862 ascaris suu
14	69.5	17.9	292	16 Q92FA8	Q92FA8 listeria in
15	69.5	17.9	300	11 Q9HY1	Q9HY1 rattus norv
16	69	17.7	190	17 Q8TQF1	Q8TQF1 methanosarc

17	69	17.7	341	3 Q12191	Q12191 saccharomyc
18	69	17.7	1430	5 Q9VMA7	Q9VMA7 drosophila
19	68.5	17.6	401	16 Q8FXH3	Q8FXH3 escherichia
20	68	17.5	574	2 Q9AJD4	Q9AJD4 streptococ
21	67.5	17.4	218	2 Q9RF14	Q9RF14 streptococ
22	67.5	17.4	1022	2 Q93T54	Q93T54 streptococ
23	67.5	17.4	1056	16 Q9PAQ0	Q9PAQ0 xylella fas
24	67.5	17.4	1876	16 Q8DQ5	Q8DQ5 streptococ
25	67	17.2	529	17 Q8TV18	Q8TV18 methanopyru
26	67	17.2	574	16 Q8P2T7	Q8P2T7 streptococ
27	67	17.2	588	2 Q9S0T6	Q9S0T6 escherichia
28	67	17.2	779	10 Q9SZB6	Q9SZB6 arabisdopsis
29	67	17.2	890	2 Q01891	Q01891 enterococcu
30	67	17.2	891	2 Q04111	Q04111 enterococcu
31	67	17.2	1433	2 Q45616	Q45616 bacillus su
32	67	17.2	1881	16 Q8RGK2	Q8RGK2 fusobacteri
33	66.5	17.1	255	16 Q9SXB4	Q9SXB4 staphylococ
34	66.5	17.1	465	2 Q9X775	Q9X775 mycoplasma
35	66.5	17.1	642	16 Q9JTL4	Q9JTL4 neisseria m
36	66.5	17.1	843	2 Q47802	Q47802 enterococcu
37	66	17.0	183	16 Q9KDD6	Q9KDD6 bacillus ha
38	66	17.0	489	17 Q8THX7	Q8THX7 methanosarc
39	66	17.0	498	16 Q8X6R2	Q8X6R2 escherichia
40	66	17.0	653	16 Q67097	Q67097 aquifex ae
41	66	17.0	1169	16 Q8K5Q0	Q8K5Q0 streptococ
42	66	17.0	1615	2 Q9KKA4	Q9KKA4 rickettsia
43	65.5	16.8	313	5 Q76641	Q76641 caenorhabdi
44	65.5	16.8	456	11 Q9CS77	Q9CS77 mus musculu
45	65.5	16.8	868	17 Q8P2M5	Q8P2M5 methanosarc

ALIGNMENTS

RESULT 1

Q53291	ID	Q53291	PRELIMINARY;	PRT;	455 AA.
AC	Q53291;				
DT	01-NOV-1996	(TEMBLrel. 01, Created)			
DT	01-NOV-1996	(TEMBLrel. 01, Last sequence update)			
DT	01-DEC-2001	(TEMBLrel. 19, Last annotation update)			
DE	Protein LG (Fragment).				
OS	Streptococcus sp.				
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC	Streptococcus.				
OX	NCBI_TaxID=1306;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93094283; PubMed=1460053;				
RA	Kihlberg B.M., Sjobring U., Kaslern W., Bjorck L.;				
RT	"Protein LG: a hybrid molecule with unique immunoglobulin binding				
RT	properties."				
RL	J. Biol. Chem. 267:25583-25588(1992).				
DR	EMBL; S50809; AAA03280.1;				
DR	HSP; P08654; IPGX.				
DR	InterPro; IPR003147; BL.				
DR	InterPro; IPR000724; Igg_bind_B.				
DR	Pfam; PF02246; B1; 4.				
DR	Pfam; PF01378; Igg-binding_B; 2.				
FT	NON_TER 455-455				
SQ	SEQUENCE 455 AA; 49926 MW; 381FC235B8C8307B CRC64;				

Query Match 100.0%; Score 389; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. NO. 2.1e-30;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	KEETPTPTDSEEVITIKANLIFANGSTOTAFKGTFEKATSEAYADTLKKNGET 60
Db	26	KEETPTPTDSEEVITIKANLIFANGSTOTAFKGTFEKATSEAYADTLKKNGET 85
Qy	61	VDVADKCYTLNIRFAG 76
Db	86	VDVADKCYTLNIRFAG 101

RESULT 2

Q51912
ID Q51912 PRELIMINARY; PRT; 719 AA.
AC Q51912;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=90215984; PubMed=2108927;
RA Kastern W., Holst E., Nielsen E., Sjoerling U., Bjorck L.;
RT "protein L, a bacterial immunoglobulin-binding protein and possible
virulence determinant";
RL J. Biol. Chem. 267:12820-12825(1992).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
DR EMBL; M86697; AAA25612.1;
DR InterPro: IPR003147; BL.
DR InterPro: IPR004829; Csurface_antigen.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR006192; LPXTG.
DR Pfam; PF02246; B1; 5.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 719 PROTEIN L.
SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100.0%; Score 389; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 3.5e-30;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 KEETPETPDSEEVTKANLIFANGSTQTAFFKGTFEKATSEAYAYADTLKKNGEY 60
|||||
98 KEETPETPDSEEVTKANLIFANGSTQTAFFKGTFEKATSEAYAYADTLKKNGEY 157
|||||
61 VDVAADKGYTLNKFAG 76
158 VDVAADKGYTLNKFAG 173

RESULT 3

Q51918
ID Q51918 PRELIMINARY; PRT; 992 AA.
AC Q51918;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;

RP SEQUENCE FROM N.A.

RC STRAIN=3316;
RX MEDLINE=95078460; PubMed=7987012;
RA Murphy J.P., Trovern A.R., Duggleby C.J.;
RT "Nucleotide sequence of the gene for peptostreptococcal protein L";
RL DNA Seq. 4:259-265(1994).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
DR EMBL; L04466; AAA67503.1;
DR HSSP; Q51911; IGAB.
DR InterPro: IPR003147; B1.
DR InterPro: IPR002988; GA.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR006192; LPXTG.
DR Pfam; PF02246; B1; 4.
DR Pfam; PF01468; GA; 4.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 992 PROTEIN L.
SQ SEQUENCE 992 AA; 108700 MW; 9CFF5771578A5DCE CRC64;

Query Match 76.7%; Score 298.5; DB 2; Length 992;
Best Local Similarity 80.3%; Pred. No. 4.7e-21;
Matches 61; Conservative 4; Mismatches 6; Indels 5; Gaps 1;
Qy 1 KEETPETPDSEEVTKANLIFANGSTQTAFFKGTFEKATSEAYAYADTLKKNGEY 60
|||||
247 EKETPE-----PEEVTKANLIFADGSGTQNAEKGTFKAYSDAYADALKKNGEY 301
Db
Qy 61 VDVAADKGYTLNKFAG 76
Db 302 VDVAADKGYTLNKFAG 317

RESULT 4

Q82EV8
ID Q82EV8 PRELIMINARY; PRT; 1576 AA.
AC Q82EV8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative hemolysin.
GN YPO2045 OR Y2267.
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Versinia pestis, the causative agent of plague";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Versinia pestis KIM."

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:02; Search time 44.137 Seconds
(without alignments)
420.957 Million cell updates/sec

Title: US-08-325-278b-1_COPY_81_152

Perfect score: 371

Sequence: 1 KEKTPPEEKEVTKANLIY.....GEYTVDDADKGYTLNKKFAG 72

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL_23.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_plant.*

10: sp_rodent.*

11: sp_virus.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archheap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	371	100.0	455	2 Q53291	Q53291 streptococ
2	371	100.0	719	2 Q51912	Q51912 peptostrept
3	308	83.0	992	2 Q51918	Q51918 peptostrept
4	98.5	26.5	216	4 Q9BPV7	Q9BPV7 homo sapien
5	98.5	26.5	398	4 Q9BP21	Q9BP21 homo sapien
6	93.5	25.2	398	11 Q9C202	Q9C202 mus musculu
7	93.5	25.2	398	11 Q91WD1	Q91WD1 mus musculu
8	89.5	24.1	1576	16 Q82EV8	Q82EV8 versinia pe
9	73	19.7	588	2 Q9S0T6	Q9S0T6 escherichia
10	70	18.9	1498	5 Q8IDP2	Q8IDP2 plasmodium
11	69.5	18.7	256	5 Q97039	Q97039 theileria p
12	69.5	18.7	256	5 Q97039	Q97039 theileria p
13	69.5	18.7	279	2 Q9ADW8	Q9ADW8 ehrlichia c
14	69.5	18.7	280	2 Q97030	Q97030 theileria c
15	69.5	18.7	451	2 Q924J9	Q924J9 lactobacill
16	69.5	18.7	623	2 Q9F4L0	Q9F4L0 fibrobacter

17	69.5	18.7	623	2 Q9F109	Q9F109 fibrobacter
18	69	18.6	529	1 Q48937	Q48937 methanosarc
19	68.5	18.5	243	17 Q9YFE6	Q9YFE6 acropyrum p
20	68.5	18.5	280	4 Q92637	Q92637 homo sapien
21	68.5	18.5	374	4 Q92663	Q92663 homo sapien
22	68.5	18.5	375	4 Q92495	Q92495 homo sapien
23	67	18.1	492	17 Q973M8	Q973M8 sulfolobus
24	67	18.1	1433	2 Q45616	Q45616 bacillus su
25	66.5	17.9	171	6 Q95N20	Q95N20 sus scrofa
26	66.5	17.9	227	6 Q95N21	Q95N21 sus scrofa
27	66.5	17.9	256	6 Q95N22	Q95N22 sus scrofa
28	66.5	17.9	333	3 Q9UVE8	Q9UVE8 yarrowia li
29	66.5	17.9	357	6 Q8SPW5	Q8SPW5 macaca fasc
30	66	17.8	448	10 Q9SKP0	Q9SKP0 arabidopsis
31	66	17.8	585	16 Q8EJH9	Q8EJH9 shewanella
32	66	17.8	873	2 Q926H6	Q926H6 lactococcus
33	65.5	17.7	108	2 P72105	P72105 neisseria m
34	65.5	17.7	496	16 Q8F022	Q8F022 leptospira
35	65.5	17.7	718	16 Q98RK2	Q98RK2 mycoplasma
36	65.5	17.7	1167	17 Q8TUJ9	Q8TUJ9 methanosarc
37	65.5	17.7	4545	2 Q9X4W2	Q9X4W2 vibrio chol
38	65.5	17.7	4558	16 Q9KS12	Q9KS12 vibrio chol
39	65	17.5	359	5 Q9VBT9	Q9VBT9 drosophila
40	65	17.5	377	16 Q8CT26	Q8CT26 staphylococ
41	65	17.5	420	5 Q8T4C5	Q8T4C5 drosophila
42	65	17.5	420	5 Q8T3P4	Q8T3P4 drosophila
43	65	17.5	425	16 Q9K491	Q9K491 streptomyce
44	64.5	17.4	188	10 Q9LEH5	Q9LEH5 hordeum vul
45	64.5	17.4	383	5 Q9VTV4	Q9VTV4 drosophila

ALIGNMENTS

RESULT 1

Q53291 ID Q53291 PRELIMINARY; PRT: 455 AA.
AC Q53291;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Protein LG (Fragment).
OS Streptococcus sp.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93094283; PubMed=1460053;
RA Kihlberg B.M., Sjobring U., Kastern W., Bjorck L.;
RT "Protein LG: a hybrid molecule with unique immunoglobulin binding properties.";
RL J. Biol. Chem. 267:25583-25588(1992).
DR EMBL; S50809; AAA03280.1; .
DR HSSP; P06654; IPOX.
DR InterPro; IPR003147; BI.
DR InterPro; IPR000724; Igc_bind_B.
DR Pfam; PF02246; BI; 4.
DR Pfam; PF01378; Igc_binding_B; 2.
FT NON_TER 455 455
SQ SEQUENCE 455 AA; 49926 MW; 381FC235B8C8307B CRC64;

Query Match 100.0%; Score 371; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.7e-29;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEEKEVTKANLIYADGKTQTAEFGTGTTEATAEAYRADALKKNGEYTVDDA 60
|||||
DB 102 KEKTPPEEKEVTKANLIYADGKTQTAEFGTGTTEATAEAYRADALKKNGEYTVDDA 161
QY 61 DKGYTLNKKFAG 72
|||||
DB 162 DKGYTLNKKFAG 173

```
RESULT 2
Q51912
ID Q51912 PRELIMINARY; PRT: 719 AA.
AC Q51912;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=90215984; PubMed=2108927;
RA Kastern W., Holst E., Nielsen E., Sjoerding U., Bjorck L.;
RT "Protein L, a bacterial immunoglobulin-binding protein and possible
virulence determinant.";
RL Infect. Immun. 58:1217-1222(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=92316971; PubMed=1618782;
RA Bjoerck L., Sjoerding U., Kastern W.;
RT "Structure of peptostreptococcal protein L and identification of
repeated immunoglobulin light chain-binding domain.";
RL J. Biol. Chem. 267:12820-12825(1992).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
DR EMBL; M86697; AAA25612.1; -.
DR InterPro: IPR003147; B1.
DR InterPro: IPR004829; Csurface_antigen.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR006192; LPXTG.
DR Pfam: PF02246; B1; 5.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR ProDom: PD153432; Csurface_antigen; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 18
FT CHAIN 19 719
FT CHAIN 19 719 POTENTIAL.
FT CHAIN 19 719 PROTEIN L.
SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100.0%; Score 371; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 8.1e-29;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTEPEKPEVTKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVA 60
DB 174 KEKTEPEKPEVTKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVA 233
QY 61 DKGYTLNKKFAG 72
DB 234 DKGYTLNKKFAG 245

RESULT 3
Q51918
ID Q51918 PRELIMINARY; PRT: 992 AA.
AC Q51918;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=90215984; PubMed=2108927;
RA Kastern W., Holst E., Nielsen E., Sjoerding U., Bjorck L.;
RT "Protein L, a bacterial immunoglobulin-binding protein and possible
virulence determinant.";
RL Infect. Immun. 58:1217-1222(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=92316971; PubMed=1618782;
RA Bjoerck L., Sjoerding U., Kastern W.;
RT "Structure of peptostreptococcal protein L and identification of
repeated immunoglobulin light chain-binding domain.";
RL J. Biol. Chem. 267:12820-12825(1992).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
DR EMBL; M86697; AAA25612.1; -.
DR InterPro: IPR003147; B1.
DR InterPro: IPR004829; Csurface_antigen.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR006192; LPXTG.
DR Pfam: PF02246; B1; 5.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR ProDom: PD153432; Csurface_antigen; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 18
FT CHAIN 19 719
FT CHAIN 19 719 POTENTIAL.
FT CHAIN 19 719 PROTEIN L.
SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100.0%; Score 371; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 8.1e-29;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTEPEKPEVTKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVA 60
DB 174 KEKTEPEKPEVTKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVA 233
QY 61 DKGYTLNKKFAG 72
DB 234 DKGYTLNKKFAG 245
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=3316;
RX MEDLINE=95078460; PubMed=7987012;
RA Murphy J.P., Trowern A.R., Duggleby C.J.;
RT "Nucleotide sequence of the gene for peptostreptococcal protein L.";
RL DNA Seq. 4:259-265(1994).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
DR EMBL; L04466; AAA67503.1; -.
DR HSSP: Q51911; 1GAB.
DR InterPro: IPR003147; B1.
DR InterPro: IPR002988; GA.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR006192; LPXTG.
DR Pfam: PF02246; B1; 4.
DR Pfam: PF01468; GA; 4.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 24
FT CHAIN 25 992
FT CHAIN 25 992 POTENTIAL.
FT CHAIN 25 992 PROTEIN L.
SQ SEQUENCE 992 AA; 108700 MW; 9CFF5771578A5DCE CRC64;

Query Match 83.0%; Score 308; DB 2; Length 992;
Best Local Similarity 84.3%; Pred. No. 2.5e-22;
Matches 59; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 KTEPEKPEVTKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVADK 62
DB 468 KTEPEKPEVTKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVADK 527
QY 63 GYTINIKFAG 72
DB 528 GYTINIKFAG 537

RESULT 4
Q9BPV7
ID Q9BPV7 PRELIMINARY; PRT: 216 AA.
AC Q9BPV7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Similar to BNS1 (BHK21) temperature sensitivity complementing.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003039; AAH03039.1; -.
DR EMBL; BC00516; AAH00516.1; -.
SQ SEQUENCE 216 AA; 24806 MW; F29028AEAC8DB04 CRC64;

Query Match 26.5%; Score 98.5; DB 4; Length 216;
Best Local Similarity 34.6%; Pred. No. 0.04;
Matches 28; Conservative 10; Mismatches 24; Indels 19; Gaps 3;

QY 3 KTEPEKPEVTKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVADK 50
DB 66 KTEPEKPEVTKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVADK 120
QY 51 DNGETYVDVADK--YTLNKK 69
DB 121 GNMKDTVDVSDMGPSHIINIK 141

RESULT 5
Q9BP21
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:02 : Search time 44.137 Seconds
(without alignments)
420.957 Million cell updates/sec

Title: US-08-325-278b-1_COPY_153_224

Perfect score: 369

Sequence: 1 KETTPPEPKEVTIKANLIY.....GKTYVDVADKGYTLNKFAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	100.0	455	Q53291	streptococc
2	369	100.0	719	Q51912	peptostrept
3	315	85.4	992	Q51918	peptostrept
4	88.5	24.0	216	Q9BPV7	homo sapien
5	88.5	24.0	398	Q9BPZ1	homo sapien
6	83.5	22.6	398	Q9CZ02	mus musculus
7	83.5	22.6	398	Q91WD1	mus musculus
8	82.5	22.4	1576	Q8ZEV8	arabidopsis
9	74	20.1	871	Q9LME2	arabidopsis
10	73.5	19.9	256	Q27039	theliera p
11	73.5	19.9	256	Q27029	theliera p
12	73.5	19.9	280	Q27030	theliera p
13	72	19.5	1025	Q9LME3	arabidopsis
14	71	19.2	265	Q23822	dualiella
15	69	18.7	324	Q9UUK3	schizosacch
16	68	18.4	448	Q9SKP0	arabidopsis

17	67.5	18.3	383	5	O9VTV4	O9vtv4 drosophila
18	67	18.2	946	2	O9EV24	O9ev24 manheimia
19	67	18.2	953	2	O9ETX2	O9etx2 manheimia
20	67	18.2	953	2	O9EV29	O9ev29 pasteurella
21	67	18.2	953	2	O9EV25	O9ev25 manheimia
22	67	18.2	953	2	O9ETG5	O9etg5 pasteurella
23	67	18.2	953	2	O9EV23	O9ev23 manheimia
24	67	18.2	953	2	O9EV34	O9ev34 pasteurella
25	67	18.2	1204	2	O8GM76	O8gm76 haemophilus
26	66.5	18.0	657	16	O92DS2	O92ds2 listeria in
27	66	17.9	477	16	O96246	O96246 arabidopsis
28	66	17.9	477	16	O8UDR8	O8udr8 agrobacteri
29	66	17.9	1096	2	O8GM79	O8gm79 haemophilus
30	66	17.9	1098	2	O48152	O48152 haemophilus
31	66	17.9	1498	5	O8IDP2	O8idp2 plasmodium
32	65.5	17.8	436	5	O21481	O21481 caenorhabdi
33	65.5	17.8	451	2	O924J9	O924j9 lactobacilli
34	65.5	17.8	476	16	O8FBV2	O8fbv2 escherichia
35	65.5	17.8	1167	17	O8TUJ9	O8tuj9 methanosarc
36	65.5	17.8	1210	2	O8GM75	O8gm75 haemophilus
37	65.5	17.8	1210	2	O8GM74	O8gm74 haemophilus
38	65.5	17.8	4545	2	O9X4W2	O9x4w2 vibrio chol
39	65.5	17.8	4558	16	O9KS12	O9ks12 vibrio chol
40	65	17.6	284	5	O76174	O76174 thelleria s
41	65	17.6	284	5	O9TYA5	O9tya5 thelleria s
42	65	17.6	636	16	O51624	O51624 borrelia bu
43	65	17.6	838	16	O84625	O84625 chlamydia t
44	64.5	17.5	243	17	O9VFE6	O9vfe6 aeropyrum p
45	64.5	17.5	333	3	O9UVE8	O9uve8 yarrowia li

ALIGNMENTS

RESULT 1

Q53291 ID Q53291 PRELIMINARY; PRT; 455 AA.
AC Q53291;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Protein LG (fragment).
OS Streptococcus sp.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae.
OC Streptococcus.
OX NCBI_TaxID=1306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93094283; PubMed=1460053;
RA Kihlberg B.M., Sjobring U., Kastern W., Bjorck L.;
RT "Protein LG: a hybrid molecule with unique immunoglobulin binding properties";
RL J. Biol. Chem. 267:25583-25588(1992).
DR EMBL; S50809; AAA03280.1; -;
DR HSSP; P06654; IpgX.
DR InterPro; IPR003147; Bl.
DR InterPro; IPR000724; Igg_bind_B.
DR Pfam; PF02246; Bl; 4.
DR Pfam; PF01378; Igg_binding_B; 2.
FT NON_TER 455 455
SQ SEQUENCE 455 AA: 49926 MW: 381FC235BBC8307B CRC64:

Query Match 100.0%; Score 369; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.4e-29;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 KETTPPEPKEVTIKANLIYADGKTQTAEFGKTFEETAEAYRYADLLAKENGYTVQVA 60
Db 174 KETTPPEPKEVTIKANLIYADGKTQTAEFGKTFEETAEAYRYADLLAKENGYTVQVA 233
QY 61 DKGYTLNKFAG 72
Db 234 DKGYTLNKFAG 245

```

RP SEQUENCE FROM N.A.
RC STRAIN-3316;
RX MEDLINE-95078460; PubMed-7987012;
RA Murphy J.P., Towern A.R., Duggieby C.J.;
RT "Nucleotide sequence of the gene for peptostreptococcal protein L.";
RL DNA Seq. 4:259-265(1994)
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
CC AN AMIDE BOND (BY SIMILARITY).
DR EMBL; L04466; AAA67503.1; -.
DR HSSP; Q51911; ICAB.
DR InterPro; IPR003147; B1.
DR InterPro; IPR002988; GA.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR006192; LPXTG.
DR Pfam; PF02246; B1; 4.
DR Pfam; PF01468; GA; 4.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25; 992 PROTEIN L.
FT SEQUENCE 992 AA; 108700 MW; 9CFF5771578A5DCE CRC64;

Query Match 85.4%; Score 315; DB 2; Length 992;
Best Local Similarity 85.7%; Pred. No. 1.9e-23;
Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0

QY 3 KTEPEEKVEVTKANLIYADGKTQTAEPKGTFEATAEAYRYADLLAKENGYTVDVADK 62
Db 468 ETPEEPKEEVTKVNLIFADGKTQTAEPKGTFEATAEAYRYADLLAKVNGEYTABLDG 527
QY 63 GYTLNIKFAG 72
Db 528 GYTLNIKFAG 537

RESULT 4
Q9BPV7 PRELIMINARY; PRT; 216 AA.
ID Q9BPV7;
AC Q9BPV7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17., Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Similar to BNS1 (BHK21) temperature sensitivity complementing.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003039; AAH03039.1; -.
DR EMBL; BC000516; AAH00516.1; -.
SQ SEQUENCE 216 AA; 24806 MW; F29028EAECA8DB04 CRC64;

Query Match 24.0%; Score 88.5; DB 4; Length 216;
Best Local Similarity 33.3%; Pred. No. 0.33;
Matches 27; Conservative 9; Mismatches 26; Indels 19; Gaps 3

QY 3 KTEPEEKVEVTKANLIYAD-----CKTQTAEEKGTFEATAEAYRYADLLAK 50
Db 66 KIKEEPKEEVTKKKEKRRDRDRQREGHGRGRPEVIOHSIFEQGPAEMMK-----KK 120
QY 51 ENGYKTYVDVADKG--YTLNIK 69
Db 121 GNWQKTVDSVDMGSPSHINIK 141

RESULT 5
Q9BP21

```

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:37 ; Search time 17.0137 Seconds
(without alignments)
406.975 Million cell updates/sec

Title: US-08-325-278B-1_COPY_153_224

Perfect score: 369

Sequence: 1 KKTPEPEPEVTIKANLIY.....GKYTVADVADKGYTLNIKFPAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	100.0	455	2 A45063	immunoglobulin-bin
2	369	100.0	719	2 A42808	ig light chain-bin
3	315	85.4	992	2 S54396	protein L precursor
4	162	43.9	74	2 A34483	ig light chain-bin
5	82.5	22.4	1576	2 AE0249	probable hemolysin
6	80.5	21.8	395	2 A43700	BNS1 protein - hum
7	74	20.1	871	2 D86355	protein T16B15.12
8	73.5	19.9	256	2 S54803	merozoite surface
9	72	19.5	1025	2 E86355	hypothetical prote
10	69	18.7	324	2 T37931	hypothetical coile
11	68	18.4	448	2 H84782	late embryogenesis
12	67	18.2	953	1 B30169	leukotoxin A - Pas
13	66.5	18.0	657	2 AD1525	probable cell surf
14	66	17.9	448	2 JC6171	late embryogenesis
15	66	17.9	470	2 AF2828	PAD dependent oxid
16	66	17.9	477	2 D97606	glycolate oxidase
17	65.5	17.8	436	2 T16638	hypothetical prote
18	65.5	17.8	476	1 W2EC	tryptophanase (sc
19	65.5	17.8	476	2 E91209	tryptophanase (imp
20	65.5	17.8	476	2 H86055	tryptophanase (imp
21	65.5	17.8	1179	2 T35033	DNA-directed DNA p
22	65.5	17.8	4558	2 C82139	RTX toxin RxaA VCI
23	65	17.6	636	2 H70184	methyl-accepting c
24	65	17.6	838	2 D71492	hypothetical prote
25	64.5	17.5	243	2 F72719	hypothetical prote
26	64	17.3	621	2 A49020	nuclear lamin C pr
27	64	17.3	722	2 T21521	hypothetical prote
28	63.5	17.2	414	2 S48738	potassium channel
29	63.5	17.2	425	2 S52852	inward rectifier p

30 63.5 17.2 479 2 T47561 late embryogenesis
31 63 17.1 88 2 C83657 hypothetical prote
32 63 17.1 319 2 H98872 hypothetical prote
33 63 17.1 693 2 E95255 choline binding pr
34 63 17.1 6642 2 T29757 protein UNC-89 - C
35 62.5 16.9 423 2 I38979 inward rectifier p
36 62.5 16.9 425 2 I48202 potassium channel-
37 62 16.8 118 2 S38717 ig heavy chain v r
38 62 16.8 195 2 A70247 conserved hypothet
39 62 16.8 356 2 T37136 hypothetical prote
40 62 16.8 529 2 S62194 hypothetical prote
41 62 16.8 1612 2 AB1347 probable peptidogl
42 61.5 16.7 266 2 A12289 hypothetical prote
43 61.5 16.7 280 2 S35103 bone sialoprotein
44 61.5 16.7 451 1 D64424 tldd homolog MU099
45 61.5 16.7 487 2 T10215 hypothetical prote

ALIGNMENTS

RESULT 1

A45063 immunoglobulin-binding protein LG - Peptostreptococcus magnus

C/Species: Peptostreptococcus magnus

C/Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999

C/Accession: A45063

R/Kihlberg, B.M.; Sjoerding, U.; Kastern, W.; Bjoerck, L.

J. Biol. Chem. 267, 25583-25588, 1992

A/Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties

A/Reference number: A45063; MUID:93094283; PMID:1460053

A/Accession: A45063

A/Status: preliminary

A/Molecule type: mRNA; protein

A/Residues: 1-455 <KIH>

A/Cross-references: GB:S50809; NID:Q261705; PIDN:AAA03280.1; PID:Q261706

A/Note: sequence extracted from NCBI backbone (NCBIN:120302, NCBIP:120303)

Query Match 100.0%; Score 369; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 6.8e-31;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTPEPEPEVTIKANLIYADGKTQTAEFKCTFEETAEAYRYADLLAKENGYTVDDVA 60
DB 174 KKTPEPEPEVTIKANLIYADGKTQTAEFKCTFEETAEAYRYADLLAKENGYTVDDVA 233

QY 61 DKGYTLNIKFPAG 72

DB 234 DKGYTLNIKFPAG 245

RESULT 2

A42808 IG light chain-binding protein precursor - Peptostreptococcus magnus

N/Alternate names: protein L

C/Species: Peptostreptococcus magnus

C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999

C/Accession: A42808; A41493

R/Kastern, W.; Sjoerding, U.; Bjoerck, L.

J. Biol. Chem. 267, 12820-12825, 1992

A/Title: Structure of peptostreptococcal protein L and identification of a repeated

A/Reference number: A42808; MUID:92316971; PMID:1618782

A/Accession: A42808

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-719 <KAS>

A/Cross-references: GB:M86697

R/Kastern, W.; Holst, E.; Nielsen, E.; Sjoerding, U.; Bjoerck, L.

Infect. Immun. 58, 1217-1222, 1990

A/Title: Protein L, a bacterial immunoglobulin-binding protein and possible virulenc

A/Reference number: A41493; MUID:90215984; PMID:2108927

A/Accession: A41493

A/Status: preliminary

probable hemolysin YPO2045 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AB0249
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice,
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan,
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barr
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AE0249
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1576 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC90857.1; PID:gl5980056; GSPDB:GN00175
C:Genetics:
A:Gene: YPO2045

Query Match 22.4%; Score 82.5; DB 2; Length 1576;
Best Local Similarity 27.5%; Pred. No. 2.4;
Matches 30; Conservative 9; Mismatches 27; Indels 43; Gaps 4;
Qy 1 KEKTPPEKPEVTIKANLIYADGKTQTAEFGKTPPEATAEAYRYADLLAKENGKTYVDVA 60
Db 1001 KANTTEQKEVSLRG-----GMTATQEIKGHLGVKAETSGDSYAEMLVGNINAKSG 1054
Qy 37 -----ATAEAYRYADLLAKENGKTYVD-----VADKGYTLNLIKFPAG 72
Db 1055 VSIKTTGDYATYATNIEGGNGDITIDAGNNLYFDQVDSORSSNIKFSG 1103

RESULT 6
A43700
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 21-Jul-2000
C:Accession: A43700
R:Ittmann, M.; Greco, A.; Basilio, C.
Mol. Cell. Biol. 7, 3386-3393, 1987
A:Title: Isolation of the human gene that complements a temperature-sensitive cell
A:Reference number: A43700; MUID:88065472; PMID:3683386
A:Accession: A43700
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-395 <ITT>
A:Cross-references: GB:ML7754; NID:gl79512; PIDN:AAA51838.1; PID:gl79513
C:Genetics:
A:Gene: GDB:BN51T
A:Cross-references: GDB:119728; OMIM:187280
A:Map position: 8pter-8q24

Query Match 21.8%; Score 80.5; DB 2; Length 395;
Best Local Similarity 32.1%; Pred. No. 0.84;
Matches 26; Conservative 9; Mismatches 27; Indels 19; Gaps 3;
Qy 3 KTPPEKPEVTIKANLIYAD-----GKTQTAEFGKTPPEATAEAYRYADLLAK 50
Db 63 KKEPEKPEVTIKKERRDRDRQEGHGRRRRPEVIQSHSIFEQGPAAEMK-----KK 117
Qy 51 ENGKTYVDVADKG--YTLNIK 69
Db 118 GNWDKTYVDVDMGPHIINIK 138

RESULT 7
D86355
protein T16B15.12 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D86355
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Ai
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewa
ansen, N.F.; Hughes, B.; Hulzar, L.

Query Match 100.0%; Score 369; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.1e-30; Indels 0; Gaps 0;
Matches 72; Conservative 0; Mismatches 0;
Qy 1 KEKTPPEKPEVTIKANLIYADGKTQTAEFGKTPPEATAEAYRYADLLAKENGKTYVDVA 60
Db 246 KEKTPPEKPEVTIKANLIYADGKTQTAEFGKTPPEATAEAYRYADLLAKENGKTYVDVA 305
Qy 61 DKGYTLNLIKFPAG 72
Db 306 DKGYTLNLIKFPAG 317

RESULT 3
A4396
protein L precursor - Peptostreptococcus magnus (strain 3316)
C:Species: Peptostreptococcus magnus
A:Variety: strain 3316
C:Date: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Oct-1999
R:Murphy, J.P.; Duggleby, C.J.; Atkinson, M.A.; Trowern, T.; Goward, C.R.
Mol. Microbiol. 12, 911-920, 1994
A:Title: The functional units of a peptostreptococcal protein L.
A:Reference number: S54396; MUID:95020613; PMID:7934898
A:Accession: S54396
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-992 <MUR>
A:Cross-references: EMBL:L04466; NID:gl50673; PIDN:AAA67503.1; PID:gl50674

Query Match 85.4%; Score 315; DB 2; Length 992;
Best Local Similarity 85.7%; Pred. No. 7.1e-25; Indels 5; Gaps 0;
Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Qy 3 KTPPEKPEVTIKANLIYADGKTQTAEFGKTPPEATAEAYRYADLLAKENGKTYVDVADK 62
Db 468 ETPPEKPEVTIKNLIFADGKTQTAEFGKTPPEATAEAYRYADLLAKENGKTYVDVAD 527
Qy 63 GYTLNLIKFPAG 72
Db 528 GYTLNLIKFPAG 537

RESULT 4
A483
light chain-binding protein L - Peptostreptococcus magnus (fragments)
C:Species: Peptostreptococcus magnus
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Aug-1996
C:Accession: A34483
R:Akerstroem, B.; Bjorck, L.
J. Biol. Chem. 264, 19740-19746, 1989
A:Title: Protein L: an immunoglobulin light chain-binding bacterial protein. Characteriz
A:Reference number: A34483; MUID:90062074; PMID:2479638
A:Accession: A34483
A:Molecule type: protein
A:Residues: 1-74 <AXE>
C:Keywords: immunoglobulin

Query Match 43.9%; Score 162; DB 2; Length 74;
Best Local Similarity 62.5%; Pred. No. 4e-10; Indels 2; Gaps 1;
Matches 35; Conservative 3; Mismatches 2; Indels 16; Gaps 1;
Qy 2 EKTPEKPEVTIKANLIYADGKTQTAEFGK-----TFPEATAEA 41
Db 9 ETTPEKPEVTIKANLIYADGKTQTAEFGKPEETPEKPEVQDGYASYEATAA 64

RESULT 5
A449

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:02 ; Search time 44.137 Seconds
(without alignments)
420.937 Million cell updates/sec

Title: US-08-325-278b-1_COPY_225_296

Perfect score: 370

Sequence: 1 KEKTEPEEKEEYIKANLIY.....GKYTADLEDGGYTNIRFAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTEMBL_23:*
- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	370	100.0	455	2 Q53291	Q53291 streptococc
2	370	100.0	719	2 Q51912	Q51912 peptostrept
3	329	88.9	992	2 Q51918	Q51918 peptostrept
4	80.5	21.8	1576	16 Q8ZEY8	Q8ZEY8 versinia pe
5	74	20.0	324	3 Q9UUK3	Q9UUK3 schizosacch
6	74	20.0	846	2 Q8RPV1	Q8RPV1 streptococc
7	71.5	19.3	216	4 Q8BPV7	Q8BPV7 homo sapien
8	71.5	19.3	398	4 Q9BP21	Q9BP21 homo sapien
9	71.5	19.3	657	16 Q92DS2	Q92DS2 listeria in
10	71	19.2	871	10 Q9LME2	Q9LME2 arabidopsis
11	70.5	19.1	256	5 Q27039	Q27039 theileria p
12	70.5	19.1	256	5 Q27029	Q27029 theileria p
13	70.5	19.1	280	5 Q27030	Q27030 theileria p
14	70.5	19.1	398	11 Q9CZ02	Q9CZ02 mus musculu
15	70.5	19.1	398	11 Q9LWD1	Q9LWD1 mus musculu
16	70	18.9	549	17 Q8TZL6	Q8TZL6 pyrococcus

17	69.5	18.8	1086	10 Q9SCU0	Q9SCU0 arabidopsis
18	69.5	18.8	1849	2 Q9SAK2	Q9SAK2 lactobacilli
19	69.5	18.8	2062	10 Q9CJ32	Q9CJ32 arabidopsis
20	69	18.6	397	16 Q92ED7	Q92ED7 listeria in
21	69	18.6	401	16 Q92ED5	Q92ED5 listeria in
22	69	18.6	1025	10 Q9LME3	Q9LME3 arabidopsis
23	68.5	18.5	858	10 Q9SGT8	Q9SGT8 arabidopsis
24	67.5	18.2	383	5 Q9VTVA	Q9VTVA drosophila
25	67	18.1	278	10 Q94KL8	Q94KL8 podophyllum
26	67	18.1	283	3 Q93337	Q93337 saccharomyc
27	66.5	18.0	1029	10 Q9SGT9	Q9SGT9 arabidopsis
28	66	17.8	495	16 Q9WGB8	Q9WGB8 staphylococ
29	65.5	17.7	225	2 Q9WX49	Q9WX49 onion yello
30	65.5	17.7	4545	2 Q9X4W2	Q9X4W2 vibrio chol
31	65.5	17.7	4558	16 Q9KSI2	Q9KSI2 vibrio chol
32	65	17.6	304	6 Q9BE26	Q9BE26 macaca fasc
33	65	17.6	319	4 Q00477	Q00477 homo sapien
34	65	17.6	334	4 Q9NR44	Q9NR44 homo sapien
35	65	17.6	334	4 Q9BU81	Q9BU81 homo sapien
36	65	17.6	357	4 Q15338	Q15338 homo sapien
37	65	17.6	359	4 P78410	P78410 homo sapien
38	65	17.6	495	4 Q9HCY1	Q9HCY1 homo sapien
39	65	17.6	513	4 Q00481	Q00481 homo sapien
40	65	17.6	584	4 Q00478	Q00478 homo sapien
41	64.5	17.4	279	2 Q9ADV8	Q9ADV8 ehrlichia c
42	64	17.3	500	16 Q8NY41	Q8NY41 staphylococ
43	64	17.3	585	16 Q8EJS9	Q8EJS9 shewanella
44	64	17.3	1433	2 Q45616	Q45616 bacillus su
45	63.5	17.2	183	16 Q8EBW9	Q8EBW9 shewanella

ALIGNMENTS

RESULT 1

Q53291 ID Q53291 PRELIMINARY; PRT; 455 AA.
AC Q53291;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Protein LG (Fragment).
OS Streptococcus sp.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae.
OC Streptococcus.
OC NCBI_TaxID=1306;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=93094283; PubMed=1460053;
RX Kihlberg B.M., Sjöbring U., Kastern W., Rjorck L.;
RT "Protein LG: a hybrid molecule with unique immunoglobulin binding properties";
RL J. Biol. Chem. 267:25583-25588(1992).
DR EMBL; S50809; AAA03280.1; -;
DR HSSP; P06654; IPGX.
DR InterPro; IPR003147; BL.
DR InterPro; IPR000724; Igg_bind_B.
DR Pfam; PF02246; BL; 4.
DR Pfam; PF01378; Igg_binding_B; 2.
FT NON_TER 455 455
SQ SEQUENCE 455 AA; 49926 MW; 381FC235BBC8307B CRC64;

Query Match 100.0%; Score 370; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 6.5e-30;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	KEKTEPEEKEEYIKANLIYADGKTQTAEKTFATAEAYRYADLLAKENGKYTAOLE 60
Db	246	KEKTEPEEKEEYIKANLIYADGKTQTAEKTFATAEAYRYADLLAKENGKYTAOLE 305
QY	61	DGGYTINIRFAG 72
Db	306	DGGYTINIRFAG 317

RESULT 2
 Q51912
 ID Q51912 PRELIMINARY; PRT; 719 AA.
 AC Q51912;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Protein L precursor.
 OS Peptostreptococcus magnus.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales;
 OC Peptostreptococcaceae; Finegoldia.
 OX NCBI_TaxID=1260;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=312;
 RX MEDLINE=90215984; PubMed=2108927;
 RA Kastern W., Holst E., Nielsen E., Sjoerding U., Bjorck L.;
 RT "Protein L, a bacterial immunoglobulin-binding protein and possible
 RL virulence determinant";
 RN Infect. Immun. 58:1217-1222(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=312;
 RX MEDLINE=92316971; PubMed=1618782;
 RA Bjoerck L., Sjoerding U., Kastern W.;
 RT "Structure of peptostreptococcal protein L and identification of
 RL repeated immunoglobulin light chain-binding domain";
 CC J. Biol. Chem. 267:12820-12825(1992).
 CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
 AN AMIDE BOND (BY SIMILARITY).
 DR EMBL; M86697; AAA25612.1;
 DR InterPro; IPR003147; B1.
 DR InterPro; IPR004829; Csurface_antigen.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR InterPro; IPR006192; LPTG.
 DR Pfam; PF02246; B1; 5.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR ProDom; PD153432; Csurface_antigen; 1.
 DR TIGRFAMs; TIGR01167; LPTG_anchor; 1.
 DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Peptidoglycan-anchor; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 719 PROTEIN L.
 SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;
 Query Match 100.0%; Score 370; DB 2; Length 719;
 Best Local Similarity 100.0%; Pred. No. 1.le-29;
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KETPEEPKEEVTIKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 60
 DB |||||
 DB 318 KETPEEPKEEVTIKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 377
 DB |||||
 DB 61 DGGYTINIRFAG 72
 DB 378 DGGYTINIRFAG 389
 RESULT 3
 Q51918
 ID Q51918 PRELIMINARY; PRT; 992 AA.
 AC Q51918;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Protein L precursor.
 OS Peptostreptococcus magnus.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales;
 OC Peptostreptococcaceae; Finegoldia.
 OX NCBI_TaxID=1260;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=312;
 RX MEDLINE=90215984; PubMed=2108927;
 RA Kastern W., Holst E., Nielsen E., Sjoerding U., Bjorck L.;
 RT "Protein L, a bacterial immunoglobulin-binding protein and possible
 RL virulence determinant";
 CC J. Biol. Chem. 267:12820-12825(1992).
 CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
 AN AMIDE BOND (BY SIMILARITY).
 DR EMBL; M86697; AAA25612.1;
 DR InterPro; IPR003147; B1.
 DR InterPro; IPR004829; Csurface_antigen.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR InterPro; IPR006192; LPTG.
 DR Pfam; PF02246; B1; 5.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR ProDom; PD153432; Csurface_antigen; 1.
 DR TIGRFAMs; TIGR01167; LPTG_anchor; 1.
 DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Peptidoglycan-anchor; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 719 PROTEIN L.
 SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;
 Query Match 100.0%; Score 370; DB 2; Length 719;
 Best Local Similarity 100.0%; Pred. No. 1.le-29;
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KETPEEPKEEVTIKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 60
 DB |||||
 DB 318 KETPEEPKEEVTIKANLIYADGKTQTAEFGTFAEATAEAYRYADLLAKENGYTADLE 377
 DB |||||
 DB 61 DGGYTINIRFAG 72
 DB 378 DGGYTINIRFAG 389
 RESULT 4
 Q8ZEVS8
 ID Q8ZEVS8 PRELIMINARY; PRT; 1576 AA.
 AC Q8ZEVS8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative hemolysin.
 GN YPO2045 OR Y2267.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Fellwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.C.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague";
 RN Nature 413:523-527(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIM5 / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM";

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:37 ; Search time 17.0137 Seconds
(without alignments)
406.975 Million cell updates/sec

Title: US-08-325-278b-1_COPY_225_296

Perfect score: 370

Sequence: 1 KEKTPPEPKKEVTIKANLIY.....CKYTADLEDGGYTINIRFAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	100.0	455	2 A45063	immunoglobulin-bin
2	370	100.0	719	2 A42808	Ig light chain-bin
3	329	88.9	992	2 S54356	protein L precursor
4	157	42.4	74	2 A34483	Ig light chain-bin
5	80.5	21.8	1576	2 AE0249	probable hemolysin
6	74	20.0	324	2 T37931	hypothetical coile
7	71.5	19.3	657	2 AD1525	probable cell surf
8	71	19.2	871	2 D86355	protein Tl6E15.12
9	70.5	19.1	256	2 S54803	merozoite surface
10	69.5	18.8	2062	2 G96602	probable receptor
11	69	18.6	397	2 AC1498	specificity determ
12	69	18.6	401	2 AE1498	specificity determ
13	69	18.6	1025	2 E86355	hypothetical prote
14	68.5	18.5	858	2 E96602	hypothetical prote
15	67	18.1	283	2 S66339	hypothetical prote
16	66.5	18.0	1039	2 E96602	hypothetical prote
17	66	17.8	495	2 D89808	hypothetical prote
18	65.5	17.7	4558	2 C82199	hypothetical prote
19	64.5	17.4	1179	2 T35093	RTX toxin REXA VC1
20	64	17.3	863	2 S06017	DNA-directed DNA p
21	64	17.3	2364	2 A56577	neuraxin - rat
22	64	17.3	2464	1 QRMSP1	microtubule-associ
23	63.5	17.2	395	2 A43700	microtubule-associ
24	63.5	17.2	550	2 A75186	BN51 protein - hum
25	63	17.0	356	2 T37136	thermosome, chain
26	63	17.0	490	2 F38462	hypothetical prote
27	63	17.0	1104	1 A36866	S-mephenytoin 4'-h
28	62.5	16.9	215	2 AC1156	microbial collagen
29	62	16.8	286	2 A12289	transcription regu
					hypothetical prote

ALIGNMENTS

RESULT 1

A45063

immunoglobulin-binding protein LG - Peptostreptococcus magnus

C:Species: Peptostreptococcus magnus

C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999

C:Accession: A45063

R:Kihlberg, B.M.; Sjobring, U.; Kastern, W.; Bjoerck, L.

J. Biol. Chem. 267, 25583-25588, 1992

A:Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties

A:Reference number: A45063; MUID:93094283; PMID:1460053

A:Accession: A45063

A:Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-455 <KIH>

A:Cross-references: GB:S50809; NID:g261705; PIDN:AAA03280.1; PID:g261706

A:Note: sequence extracted from NCBI backbone (NCBIN:120302, NCBIP:120303)

Query Match: 100.0%; Score 370; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 4.3e-32;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEPKGFATATAYRYADLLAKENGYKTADLE 60

Db 246 KEKTPPEPKKEVTIKANLIYADGKTQTAEPKGFATATAYRYADLLAKENGYKTADLE 305

Qy 61 DGGYTINIRFAG 72

Db 306 DGGYTINIRFAG 317

RESULT 2

A42808

Ig light chain-binding protein precursor - Peptostreptococcus magnus

N:Alternate names: protein L

C:Species: Peptostreptococcus magnus

C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999

C:Accession: A42808; A41493

R:Kastern, W.; Sjoebing, U.; Bjoerck, L.

J. Biol. Chem. 267, 12820-12825, 1992

A:Title: Structure of peptostreptococcal protein L and identification of a repeated

A:Reference number: A42808; MUID:92316971; PMID:1618782

A:Accession: A42808

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-719 <KAS>

A:Cross-references: GB:M86697

R:Kastern, W.; Holst, E.; Nielsen, E.; Sjoebing, U.; Bjoerck, L.

Infect. Immun. 59, 1217-1222, 1990

A:Title: Protein L, a bacterial immunoglobulin-binding protein and possible virulence

A:Reference number: A41493; MUID:90215984; PMID:2108927

A:Accession: A41493

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 202-275 <KA2>
C:Keywords: immunoglobulin

Query Match 100.0%; Score 370; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 7.2e-32;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KETPEEPKEEVIKANIYADGKTQTAEFGKTFATAEAYRYADLLAKENGYTADLE 60
|||||
Db 318 KETPEEPKEEVIKANIYADGKTQTAEFGKTFATAEAYRYADLLAKENGYTADLE 377
|||||
QY 61 DGGYTINIRFAG 72
|||||
Db 378 DGGYTINIRFAG 389
|||||

RESULT 3

S54396
Protein L precursor - Peptostreptococcus magnus (strain 3316)
C:Species: Peptostreptococcus magnus
C:Accession: S54396
C:Date: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Oct-1999
R:Murphy, J.P.; Duggleby, C.J.; Atkinson, M.A.; Trowern, A.R.; Atkinson, T.; Goward, C.R.
Mol. Microbiol. 12, 911-920, 1994
A:Title: The functional units of a peptostreptococcal protein L.
A:Reference number: S54396; MUID:95020613; PMID:7934898
A:Accession: S54396
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-992 <MUR>
A:Cross-references: EMBL:L04466; NID:g150673; PIDN:AAA67503.1; PID:g150674

Query Match 88.9%; Score 329; DB 2; Length 992;
Best Local Similarity 90.0%; Pred. No. 2.7e-27;
Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 3 KETPEEPKEEVIKANIYADGKTQTAEFGKTFATAEAYRYADLLAKENGYTADLE 62
|||||
Db 468 ETPEEPKEEVIKNIYLFADGKTQTAEFGKTFEATAEAYRYADLLAKVNGEYTDLE 527
|||||
QY 63 GYTINIRFAG 72
|||||
Db 528 GYTINIRFAG 537
|||||

RESULT 4

A34483
light chain-binding protein L - Peptostreptococcus magnus (fragments)
C:Species: Peptostreptococcus magnus
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Aug-1996
C:Accession: A34483
R:Akerstrom, B.; Bjoerck, L.
J. Biol. Chem. 264, 19740-19746, 1989
A:Title: Protein L: an immunoglobulin light chain-binding bacterial protein. Characterization of the protein L gene.
A:Reference number: A34483; MUID:90062074; PMID:2479638
A:Accession: A34483
A:Molecule type: protein
A:Residues: 1-74 <AKE>
C:Keywords: immunoglobulin

Query Match 42.4%; Score 157; DB 2; Length 74;
Best Local Similarity 62.7%; Pred. No. 4.8e-10;
Matches 37; Conservative 2; Mismatches 10; Indels 10; Gaps 2;

QY 2 EKTPEEPKEEVIKANIYADGKTQTAEFGKTFATAEAYRYADLLAKE 51
|||||
Db 9 ETTPEEPKEEVIKANIYADGKTQTAEFGKTFEATAEAYRYADLLAKVNGEYTDLE 66
|||||

probable hemolysin YPO2045 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: A50249
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan
II, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Bar
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: A50249
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1576 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC90857.1; PID:g15980056; GSPDB:GN00175
C:Genetics:
A:Gene: YPO2045

Query Match 21.8%; Score 80.5; DB 2; Length 1576;
Best Local Similarity 25.7%; Pred. No. 2.6;
Matches 28; Conservative 13; Mismatches 25; Indels 43; Gaps 4;
QY 1 KETPEEPKEEVIKANIYADGKTQTAEFGKTFATAEAYRYADLLAKENGYTADLE 36
|||||
Db 1001 KANTTEQKEVSLRG-----GMTATQETKGLGVKAETSQGDSYAEMLVGNINAKSG 1054
|||||
QY 37 ---ATAEAYRYADLLAKENGYTAD-----LEDGGYTINIRFAG 72
|||||
Db 1055 VSIKTTGDVYYATNIEGGNGDITDAGNNLYFDQVDQSORSNNIKESG 1103
|||||

RESULT 6

T37931
hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T37931
R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A:Reference number: 221755
A:Accession: T37931
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-324 <MCD>
A:Cross-references: EMBL:AL109820; PIDN:CAB52567.1; GSPDB:GN00066; SPDB:SPAC1952.0
A:Experimental source: strain 972h-; cosmid C1952
C:Genetics:
A:Gene: SPDB:SPAC1952.03
A:Map position: 1
A:Introns: 144/3

Query Match 20.0%; Score 74; DB 2; Length 324;
Best Local Similarity 30.2%; Pred. No. 2.2;
Matches 19; Conservative 14; Mismatches 26; Indels 4; Gaps 1;

QY 1 KETPEEPKEEVIKANIYADGKTQTAEFGKTFATAEAYRYADLLAKENGYTADLE 60
|||||
Db 126 KENTPOQPKSRNRQKERL----ERRKAEMKMSQAELSEKMAADLKNEKKKFSKILE 181
|||||
QY 61 DGG 63
Db 182 EAG 184

RESULT 7

AD1525
probable cell surface protein (LPXTG motif) [imported] - Listeria innocua (strain C)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AD1525
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blic
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fslf
D.; Jones, L.M.; Karst, U.